

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: September 7, 2002, 22:32:16 ; Search time 1837.47 Seconds
(without alignments)
1378.042 Million cell updates/sec

Title: US-09-719-017A-1
Perfect score: 121
Sequence: 1 gaattccctgtgacaatca.....tatctaagaagaacttaca 121

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1797656 segs, 10463268293 residues
Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
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6: gb_pat:*
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33: em_htgo_inv:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result, being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match	Length	DB ID	Description
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1	121	100.0	121	6	AX008752	Sequence 121 bp	DNA	linear	PAT 06-SEP-2000
2	121	100.0	1793	6	AX008753	Sequence 1 from Patent WO9964607.			
3	121	100.0	1793	6	AX025996				
4	92.8	76.7	118	6	A06104	Insertion f			
5	92.8	76.7	118	6	A09134	Nucleotide			
6	79.4	65.6	215	6	A03764	Synthetic (
7	47	38.8	146	6	A29213	Synthetic D			
8	43.6	36.0	90	6	E00407	DNA coding			
9	43.6	36.0	357	6	AR172799	Sequence			
10	43.6	36.0	357	6	BD000394	DNA encod			
11	43.2	35.7	1519	6	E31303	Process for			
12	43	35.5	262	1	ECOTRPRO				
13	43	35.5	269	12	SYNDVA				
14	42.8	35.4	63	6	E00405	DNA coding			
15	42.4	35.0	44	6	A12512	trp promote			
16	42.2	34.9	118	6	A17072	oligonucleo			
17	42.2	34.9	118	6	A17463	oligonucleo			
18	42.2	34.9	118	6	A23882	oligonucleo			
19	42.2	34.9	118	6	AR014440	Sequence			
20	42.2	34.9	118	6	AR059827	Sequence			
21	42.2	34.9	118	6	I11886	Sequence 53			
22	42.2	34.9	305	6	A76225	Sequence 17			
23	42	34.7	47	6	A11701	oligonucleo			
24	42	34.7	47	6	A15884	oligonucleo			
25	42	34.7	74	6	A24959	trp operon			
26	42	34.7	74	6	A27465	oligonucleo			
27	42	34.7	74	6	A27466	oligonucleo			
28	42	34.7	74	23	A20751	oligonucleo			
29	42	34.7	78	6	E00333	trp promote			
30	42	34.7	78	6	I04258	Sequence 2			
31	42	34.7	84	6	A15698	trp promote			
32	42	34.7	86	6	A15697	trp promote			
33	42	34.7	99	6	A15714	PMT 501 Hae			
34	42	34.7	101	6	A15715	oligonucleo			
35	42	34.7	103	6	A15336	Synthetic t			
36	42	34.7	103	6	I06143	Sequence 33			
37	42	34.7	103	6	I07537	Sequence 33			
38	42	34.7	103	6	I08035	Sequence 11			
39	42	34.7	103	6	I08091	Sequence 6			
40	42	34.7	103	6	I08582	Sequence 31			
41	42	34.7	103	6	I09296	Sequence 9			
42	42	34.7	105	6	A15335	Synthetic t			
43	42	34.7	105	6	E01081	DNA sequenc			
44	42	34.7	105	6	E01711	DNA sequenc			
45	42	34.7	105	6	E01714	DNA sequenc			

ALIGNMENTS

RESULT 1
AX008752 121 bp DNA linear PAT 06-SEP-2000
LOCUS AX008752
DEFINITION Sequence 1 from Patent WO9964607.
ACCESSION AX008752
VERSION AX008752.1 GI:9996243
KEYWORDS
SOURCE
ORGANISM Escherichia coli.
Escherichia coli.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae; Escherichia.

REFERENCE 1 (bases 1 to 121)
AUTHORS Favre-Bulle,O., Guitton,C. and Pierrard,J.
TITLE Industrial method for producing heterologous proteins in e.coli and strains useful for said method
JOURNAL Patent: WO 9964607-A 1 16-DEC-1999;
FAVRE BULLE OLIVIER (FR); GUITTON CAROLE (FR); PIERRARD JEROME (FR); RHONE POULENC NUTRITION ANIMAL (FR)
FEATURES
source
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/organism="Escherichia coli"
/db_xref="taxon:562"

BASE COUNT 37 a 27 c 23 g 34 t

ORIGIN

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Best Local Similarity 100.0%; Pred. No. 6.3e-32;

Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 GAATTCCTGTGACAAATTAATCATCGAAGTAACTAGTACCGACCTGGCTGCAGG 60
QY 61 tcgacctgagccaaagcttgggcatacatcaatcaatgttactaaggaaacttac 120
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DB 61 TCGACCTGCAGCCAACTGGGCATCATCATCATCTGTATCTAAGAAATACTTAC 120
QY 121 a 121
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DB 121 A 121

RESULT 2

AX008753 1793 bp DNA linear PAT 06-SEP-2000
LOCUS Sequence 2 from Patent WO9964607.
DEFINITION AX008753
ACCESSION AX008753
VERSION AX008753.1 GI:9996244
KEYWORDS
SOURCE
ORGANISM
synthetic construct.
artificial sequence.

REFERENCE 1 (bases 1 to 1793)
Favre-Bulle,O., Guitton,C. and Pierrard,J.
AUTHORS Industrial method for producing heterologous proteins in e.coli and
TITLE strains WO 9964607-A 2 16-DEC-1999;
JOURNAL PATENT: BULE OLIVIER (FR); GUITTON CAROLE (FR); PIERREARD JEROME
(FR); RHONE POULENC NUTRITION ANIMAL (FR)

FEATURES

source

1..1793
Location/Qualifiers
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="cassette d'expression"
123..1193
/note="unnamed protein product"
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/transl_table=11
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/db_xref="GI:9996245"
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FGEWLPDYPFHWLIGAPAWMSLKYSARYANSLSDSAEFORIAOAAATLGIPTALGY
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LCWEHLSPKSLVALYSQHEALHIAAMPSEFLYSQAHALSAKVMMAASQIYSVEGQC
FTIASSVYVDETLDMEVGEHNASLKVGGSSMIFAPDGRTLAPYLPHDAEGILIA
DLMEEIAFAKAIINDPVGHYSKPEATRLVLDLGHREPMTRVHRSKSVIOEAEPEPHVOS
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CDS

BASE COUNT 412 a 527 c 478 g 376 t
ORIGIN

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Best Local Similarity 100.0%; Pred. No. 9.9e-32;

Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 tcgacctgagccaaagcttgggcatacatcaatcaatgttactaaggaaacttac 120
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DB 61 TCGACCTGCAGCCAACTGGGCATCATCATCATCTGTATCTAAGAAATACTTAC 120
QY 121 a 121
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1

DB 121 A 121

RESULT 3

AX025996 1793 bp DNA linear PAT 16-SEP-2000
LOCUS Sequence 1 from Patent FR2787121.
DEFINITION AX025996
ACCESSION AX025996
VERSION AX025996.1 GI:10187454
KEYWORDS
SOURCE
ORGANISM

Alcaligenes faecalis.
Alcaligenes faecalis.
Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
Alcaligenes.

REFERENCE 1 (bases 1 to 1793)
Favre,B.O., Pierrard,J. and Batisse,D.N.
AUTHORS Patent: FR 2787121-A 1 16-JUN-2000;
JOURNAL AVENTIS CROSCIENCE (FR)

FEATURES

source

1..1793
Location/Qualifiers
/organism="Alcaligenes faecalis"
/db_xref="taxon:511"
123..1193
/note="unnamed protein product"
/codon_start=1
/transl_table=11
/protein_id="CAC09069.1"
/db_xref="GI:10187455"
/translation="MOTRKIVRAAVQASPNYDLATGVDKTIELARQARDEGCDLIY
FGEWLPDYPFHWLIGAPAWMSLKYSARYANSLSDSAEFORIAOAAATLGIPTALGY
SERSGSLYLGGCLIDDKGOMLSRRKLPKHVEFTVGEGRADLIYSDPELGRVGA
LCWEHLSPKSLVALYSQHEALHIAAMPSEFLYSQAHALSAKVMMAASQIYSVEGQC
FTIASSVYVDETLDMEVGEHNASLKVGGSSMIFAPDGRTLAPYLPHDAEGILIA
DLMEEIAFAKAIINDPVGHYSKPEATRLVLDLGHREPMTRVHRSKSVIOEAEPEPHVOS
TAAPVAVSQTQSDTLVQEPS"

CDS

BASE COUNT 412 a 527 c 478 g 376 t
ORIGIN

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Best Local Similarity 100.0%; Pred. No. 9.9e-32;

Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gaattccctgtgacaataatcatcgaactagtagtaactagtagcgaactgtgctgagg 60
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DB 1 GAATTCCTGTGACAAATTAATCATCGAAGTAACTAGTACCGACCTGGCTGCAGG 60
QY 61 tcgacctgagccaaagcttgggcatacatcaatcaatgttactaaggaaacttac 120
|||||
DB 61 TCGACCTGCAGCCAACTGGGCATCATCATCATCTGTATCTAAGAAATACTTAC 120
QY 121 a 121
|
DB 121 A 121

RESULT 4

A06104 118 bp DNA linear PAT 18-MAY-1993
LOCUS Insertion fragment to produce pfc80.
DEFINITION A06104
ACCESSION A06104
VERSION A06104.1 GI:345112
KEYWORDS
SOURCE
ORGANISM

synthetic construct.
synthetic construct
artificial sequence.

REFERENCE 1 (bases 1 to 118)
NEW DERIVATIVES OF HUMAN/BOVINE BASIC FIBROBLAST GROWTH FACTOR
TITLE Patent: WO 9002800-A 10 22-MAR-1990;
JOURNAL Location/Qualifiers
FEATURES 1..118
source /organism="synthetic construct"

PN	JP	2000325090-A/2
PD	28-NOV-2000	
PF	15-MAR-2000	JP 2000071879
PR		
PI	TAIKI NINOMIYA, TETSUYA MIWA, MINAO ASANO, NAMI NAKAMURA, PI	
TSUNEKI	NIO	
PC	C12N15/09, C12N1/15, C12N1/19, C12N1/21, C12N5/10, PC	
C12N9/48///A23L1/238,		
PC	C12N15/00, C12N5/00	
CC		
Key		
FT	promoter	Location/Qualifiers
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/organism="synthetic construct"
/db_xref="taxon:32630"

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Best Local Similarity	92.0%;	Prod No 0.00015;		

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11		
51	320	
E31303		
10000		

LOCUS	E31303	1519 bp	DNA	linear	PAT 07-FEB-2001
DEFINITION	Sequence for producing novel microbial transglutaminase.				
ACCESSION	E31303				
VERSION	E31303.1	GI:13025693			
KEYWORDS	JP 1999075876-A/2.				
SOURCE	unidentified.				
ORGANISM	unidentified.				
REFERENCE	1 (bases 1 to 1519)				
AUTHORS	Kellichi,Y.N.N.N. and Miwa,K.S.				
TITLE	Process for producing novel microbial				
JOURNAL	Patent: JP 1999075876-A 2 23-MAR-1999.				

COMMENT
OS Unidentified
PN JP 199075876-A/2
PD 23-MAR-1999
PF 29-JUN-1998 JP 1998181951
PR

PC KEIICHI YOKOYAMA, NAMI NAKAMURA, TETSUO MINA, KATSUYA SEGURO PC
C12N15/09, C12N1/21, C12N9/10// (C12N1/21, C12R1:19), (C12N9/10, PC
C12R1:19),
PC C12N15/00

FEATURES	source	Location/Qualifiers
FT	Key	Location/Qualifiers
CDS		87. .1082.
		Location/Qualifiers
		1. .1519

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/db_xref="taxon:32644"
BASE COUNT      355 a      350 c      387 g      427 t
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Query Match	35.74;	Score 43.2;	DB 6;	Length 1519;
Best Local Similarity	93.88;	Pred. No. 0.00026;		
Matches 45;	Conservative 0;	Mismatches 3;	Indels 0;	Gaps 0

2 TCCCCTGTGACAAATTATCATCGAAGTAACTAGTAGACCAAGTT 49

2 TCCCCTGTGACAAATTATCATCGAAGTAACTAGTAGACCAAGTT 49

RESULT 12
ECOTRPPRO 62 bp DNA linear BCT 26-APR-1993
LOCUS E.coli trp promoter region.
DEFINITION K01792.1 GI:148058
ACCESSION K01792.1 GI:148058
VERSION mutational analysis; promoter region; trp operon.
KEYWORDS E.coli DNA.
SOURCE Escherichia coli
ORGANISM Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
REFERENCE 1 (bases 1 to 62)
AUTHORS Russell,D.R. and Bennett,G.N.
TITLE Construction and analysis of in vivo activity of E. coli promoter
JOURNAL hybrids and promoter mutants that alter the -35 to -10 spacing
MEDLINE Gene 20, 231-243 (1982)
COMMENT [1] examines the efficiency of gene expression in E.coli if the
distance between the -35 and -10 regions is increased and also when
the -35 region from one and the -10 region from another gene are
recombined to form a hybrid promoter region. In every case it was
found that the spacing between these two regions was of prime
importance and can not be greater than 18 bp in a functional
promoter.
FEATURES
source Location/Qualifiers
1..62
-35_signal /organism="Escherichia coli"
-10_signal /db_xref="taxon:562"
BASE COUNT 43. 25
17 a 19 c 10 g 16 t
ORIGIN 27.7 min on K12 map.
Query Match 35.5%; Score 43; DB 1; Length 62;
Best Local Similarity 100.0%; Pred. No. 0.00018;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 15 CCCTGTTGACATTAATCATCGAAGTAACTAGTACGACG 57
RESULT 13
SYNDVA 269 bp DNA linear SYN 27-APR-1993
LOCUS SYNDVA
DEFINITION Synthetic plasmid pSL1 DNA fragment.
ACCESSION M31473
VERSION M31473.1 GI:208822
KEYWORDS
SOURCE Synthetic DNA, clone pSL1.
ORGANISM unidentified cloning vector.
REFERENCE 1 (bases 1 to 269)
AUTHORS Laflamme,S.E., Kramer,F.R. and Mills,D.R.
TITLE Comparison of pausing during transcription and replication
JOURNAL Nucleic Acids Res. 13, 8425-8440 (1985)
MEDLINE 86093652
FEATURES
source Location/Qualifiers
1..269
/organism="unidentified cloning vector"
/db_xref="taxon:45196"
BASE COUNT 49 a 92 c 83 g 45 t
ORIGIN
Query Match 35.5%; Score 43; DB 12; Length 269;
Best Local Similarity 100.0%; Pred. No. 0.00023;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 6 ccctgttgacaataatcgcactagtaactagtagcag 48
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DB 7 CCCTGTTGACATTAATCATCGAAGTAACTAGTACGACG 49
RESULT 14
E00405 63 bp RNA linear PAT 29-SEP-1997
LOCUS E00405
DEFINITION DNA coding for trp promoter.
ACCESSION E00405
VERSION E00405.1 GI:216868
KEYWORDS JP 1985160887-A/1
SOURCE unidentified plasmid.
ORGANISM unidentified plasmid
plasmids.
REFERENCE 1 (bases 1 to 63)
AUTHORS Nakagawa,Y., Uno,S., Nagai,M. and Aritmura,H.
TITLE VECTOR
JOURNAL Patent: JP 1985160887-A 1 22-AUG-1985;
COMMENT GREEN CROSS CORP:THE
OS plasmid
PN JP 1985160887-A/1
PD 22-AUG-1985
PF 02-FEB-1984 JP 198401813
PI NAKAGAWA YUKIMITSU, UNO SHUSEI, NAGAI MASANORI, PI ARIMURA
HIROBUMI
PC C12N15/00//C07H21/04;
CC strandedness: Single;
CC topology: Linear;
CC hypothetical: No;
FH key Location/Qualifiers
FH
FT -35_signal 5. 10
FT -10_signal 28. 33
FT RBS 57. 60.
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source Location/Qualifiers
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/organism="unidentified plasmid"
/db_xref="taxon:45202"
BASE COUNT 22 a 13 c 11 g 17 t
ORIGIN
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Best Local Similarity 95.7%; Pred. No. 0.00021;
Matches 44; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
DB 6 ccctgttgacaataatcgcactagtaactagtagcagct 51
|||||
DB 1 CCCTGTTGACATTAATCATCGAAGTAACTAGTACGACGAGTT 46
RESULT 15
A12512 44 bp DNA linear PAT 05-JAN-1994
LOCUS A12512
DEFINITION trp promoter and transcriptional start site.
ACCESSION A12512
VERSION A12512.1 GI:491382
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 44)
AUTHORS
TITLE TRANSLATION OF mRNA
JOURNAL Patent: WO 8707644-A 19 17-DEC-1987;
MEDLINE
FEATURES
source Location/Qualifiers
1..44
/organism="synthetic construct"
/db_xref="taxon:32630"
BASE COUNT 15 a 8 c 7 g 14 t
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Query Match 35.0%; Score 42.4; DB 6; Length 44;
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Best Local Similarity 97.7%; Pred. No. 0.00027;
 Matches 43; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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 Db 1 CTGTTGACAAATTAATCATCGAACTAGTACTAGTACGAAGCTT 44

Search completed: September 8, 2002, 00:37:47
 Job time: 7531 sec